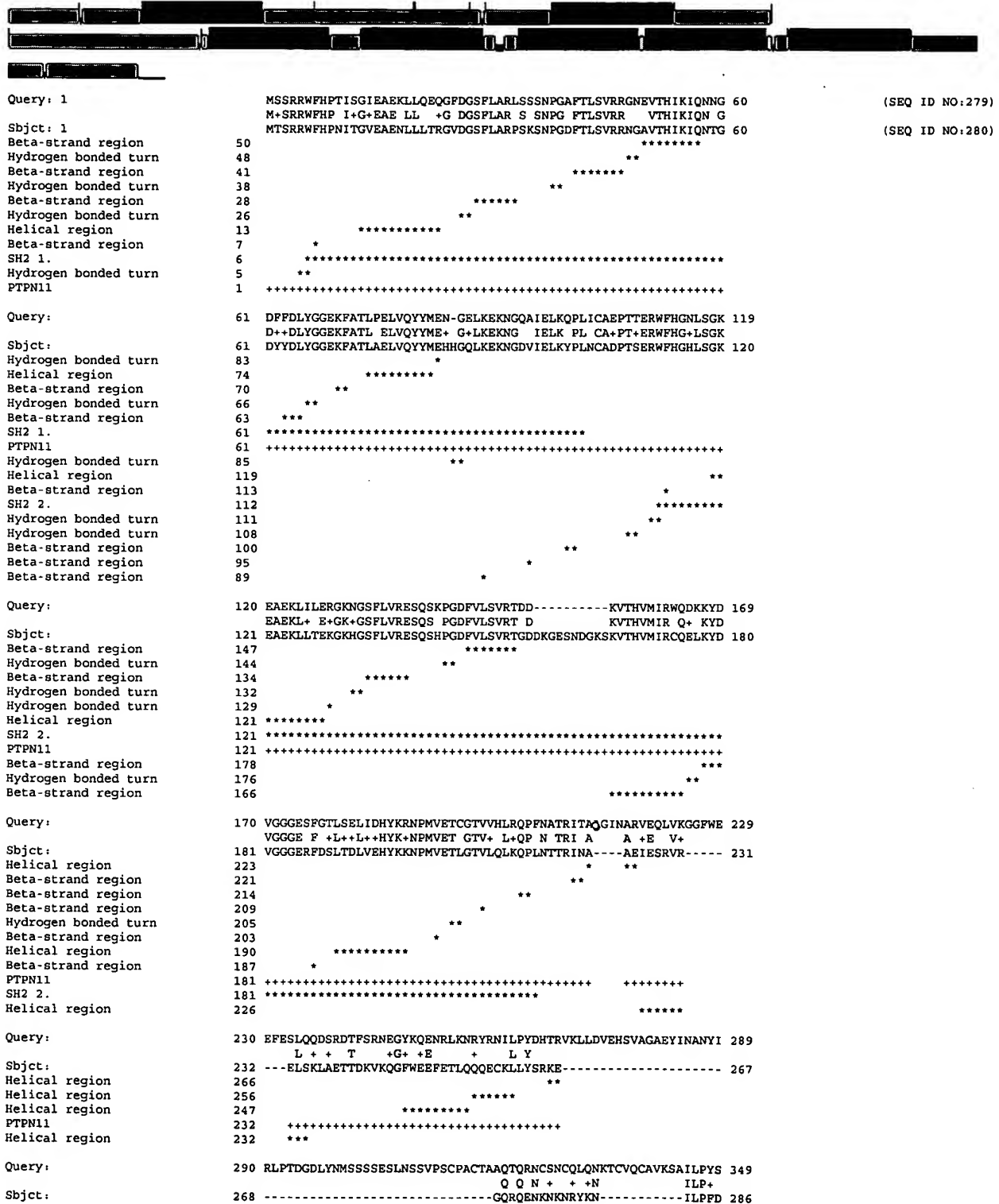


REPLACEMENT SHEET

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FIGURE 2

Score = 553 bits (1425), Expect = e-156
Identities = 327/700 (46%), Positives = 406/700 (57%), Gaps = 152/700 (21%)



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```
Hydrogen bonded turn      280
PROTEIN-TYROSINE PHOSPHATASE. 276
Helical region            271
PTPN11                    268
Helical region            268
Hydrogen bonded turn      286

Query:                    350 NCATCSRKSDLSLKHKRSESSASSPSSGSGSGPGSSGTSVSVNGPGTPTNLTSGTAG 409
+ D P P +
Sbjct:                    287 HTRVVLHDGD-----PNEPVS----- 302
Beta-strand region        289 ***
Hydrogen bonded turn      287 **
PTPN11                    287 ++++++++
PROTEIN-TYROSINE PHOSPHATASE. 287 *****

Query:                    410 CLVGLLKRHSNDSSGAVSISMAERERE-REREMFKTYIATQGCLLTQQVNTVTDFWNMVW 468
D A + I M E E + + K+YIATQGCL NTV DFW MV+
Sbjct:                    303 -----DYINA-NIIMPEFETKCNNSKPKKSYIATQGCLQ-----NTVNDPWRMV 346
Beta-strand region        304 *****
PTPN11                    303 ++++++
PROTEIN-TYROSINE PHOSPHATASE. 303 *****
Hydrogen bonded turn      335 *
Beta-strand region        327 ****
Helical region            338 *****

Query:                    469 QENIRVIVMTTKEYERGKEKCARYWPDEGRSEQFGHARIQCVSENSTSDYTLREFLVSWR 528
QEN+RVIVMTTKE ERGK KC +YWPDE ++G R++ V E++ DYTLRE +S
Sbjct:                    347 QENSRVIVMTTKEVERGKSKCVKYPDEYALKEYGVMVRNVKESAAHDYTLRELKLSKV 406
Hydrogen bonded turn      406 *
Beta-strand region        396 *****
Beta-strand region        383 *****
Hydrogen bonded turn      381 **
Beta-strand region        377 ****
Hydrogen bonded turn      374 **
Beta-strand region        364 **
Hydrogen bonded turn      362 **
Beta-strand region        360 **
Beta-strand region        352 ****
Hydrogen bonded turn      349 *
Helical region            347 **
PTPN11                    347 ++++++++
PROTEIN-TYROSINE PHOSPHATASE. 347 *****

Query:                    529 DQ--PARRIFHYHFQVWPDHGVDPADPGCVLNFQDVNTRQSHLAQAGEKPGPICVHCSAG 586
Q R ++ YHF+ WPDHGVDP+DPG VL+FL+V+ +Q + AG P+ VHCSAG
Sbjct:                    407 GQGNTERTVWQYHFRTPDHDGVPSDPGGVLDLFLEEVHKKQESIMDAG----PVVVHCSAG 462
Beta-strand region        408 *****
Hydrogen bonded turn      407 *
PTPN11                    407 ++++++++
PROTEIN-TYROSINE PHOSPHATASE. 407 *****
Hydrogen bonded turn      450 **
Helical region            432 *****
active                    459 *
Beta-strand region        455 ****

Query:                    587 IGRTGTFIVIDMILDQIVRNLDTEDIQRTIQMVRQRSGLVQTEAQYKFVYAVQHYI 646
IGRTGTFIVID++D I G+D +ID+ +TIQMVRQRSG+VQTEAQY+F+Y AVQHYI
Sbjct:                    463 IGRTGTFIVIDILIDIIREKGVDCIDVPKTIQMVRQRSGMVQTEAQYRFIYMAVQHYI 522
Helical region            508 *****
Hydrogen bonded turn      502 **
Hydrogen bonded turn      499 **
Helical region            490 *****
Beta-strand region        487 **
Hydrogen bonded turn      484 **
Helical region            464 *****
PTPN11                    463 ++++++++
PROTEIN-TYROSINE PHOSPHATASE. 463 *****

Query:                    647 QTLIARKRAEEQSLQVGREYTNIKYTGEIGNDSQRSPLPP 686
+TL R E++S + G EYTNIKY+ +SPLPP
Sbjct:                    523 ETLQRRIEEEQSKRKRGHEYTNIKYSLADQTSQDQSPPLPP 562
Conflict                    548 *
phosphorylation            542 *
Conflict                    535 *
Hydrogen bonded turn      524 *
Helical region            523 *
PTPN11                    523 ++++++++
```

REPLACEMENT SHEET

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FIGURE 6A

Sequence alignment of Dros Dlg1 and Hu Dlg homolog 1

BLAST P sequence alignment

Score = 616 bits (1588), Expect = e-175
Identities = 306/517 (59%), Positives = 390/517 (75%), Gaps = 24/517 (4%)



```

Query: 453 QPGSRYASTNVLAAPPGTPRAVST-----EDITREPTITIQKGPQGLGFNIVGGE 504      (SEQ ID NO:281)
          QP  + S +      P +P S      ++ITREPR + + +G GLGFNIVGGE
Sbjct: 425 QPVDNHVSPSSFLGQTPASPARYSPVSKAVLGDDDEITREPRKVVLRHGSTGLGFNIVGGE 484      (SEQ ID NO:282)

Query: 505 DGQGIYVSFILAGGPADLGSELKRGDQLLSVNNVNLTHATHEEAAQALKTSGGVVTLAQ 564
          DG+GI++SFILAGGPADL EL++GD+++SVN+V+L A+HE+AA ALK +G VT++AQ
Sbjct: 485 DGEGIFISFILAGGPADLSGELKRGDRIISVNSVDLRAASHEQAAAALKNAGQAVTIVAQ 544

Query: 565 YRPEEYNRFEARIQELKQXXXXXXXXXXXXXX-XXQKRSLYVRALFDYDPNRDDGLPSRG 623
          YRPEEY+RFEA+I +L++Q      QKRSLYVRALFDYD +D GLPS+G
Sbjct: 545 YRPEEYSRFEAKIHDLRQMMNSSISSGSGSLRTSQKRSLYVRALFDYDKTKDSGLPSQG 604

Query: 624 LPFKHGDILHVTNASDDEWQARRVLGDNEDEQIGIVPSKRRWERKMRARDRSVKFQGHA 683
          L FK GDILHV NASDDEWQAR+V D E +++G++PSKRR E+K RAR ++VKF
Sbjct: 605 LNFKFGDILHVINASDDEWQARQVTPDGESDEVGVIPSKRRVEKKERARLKTVKFN--- 661

Query: 684 AANNLNDKQSTLDRKKKNFTFSRKFPFMKSRDEKNEDGSDQEPNGVVSSTSEIDIXXXXX 743
          + DK + + K+K FSRKFPP K++D+ ++ SD + + V S+ S+ +
Sbjct: 662 --SKTRDKQSFNDKRKKNLFSRKFPFYKNKDQSEQETSDADQH-VTSNASDSE----- 712

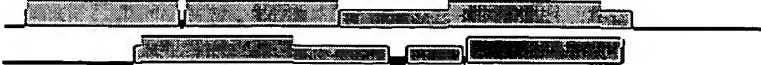
Query: 744 XXXXXXXXXXXXXVLSYEAQRLSINYTRPVIILGPLKDRINDDLISEYDPDKFGSCVPHTT 803
          VLSYE V + +NYTRPVIILGP+KDRINDDLISE+PDKFGSCVPHTT
Sbjct: 713 ---SSYRQGEYVLSYEPVNQEVNYTRPVIILGPMKDRINDDLISEFPDKFGSCVPHTT 769

Query: 804 RPKREYEVDGRDYHFVSSREQMERDIQNHLFIEAGQYNDNLYGTSVASVREVAEKGKHCI 863
          RPKR+YEVDGRDYHFV+SREQME+DIQ H FIEAGQYN++LYGTSV SVREVA KGKHCI
Sbjct: 770 RPKRDYEVDGRDYHFVTSREQMEKDIQEHKFIEAGQYNNHLYGTSVQSVREVAGKGKHCI 829

Query: 864 LDVSGNAIKRLQVAQLYPVAVFIKPKSVDSVMEMNRRMTTEEAKKTYERAIKMEQEFGEY 923
          LDVSGNAIKRLQ+AQLYP+++FIKPKS+++MEMN+R+TEEA+KT+ERA+K+EQEF E+
Sbjct: 830 LDVSGNAIKRLQIAQLYPISIFIKPKSMENIMEMNKRLTEEQARKTFERAMKLEQEFT 889

Query: 924 FTGVVQGDITIEEYISKVKSMIWSQSGPTIWVPSKESL 960
          FT +VQGDT+E+IY++VK +I QSG IWVP+KE L
Sbjct: 890 FTAIVQGDITLEDIYNQVKQIIEEQSGSYIWVPAKEKL 926
Score = 206 bits (524), Expect = 2e-51
Identities = 119/227 (52%), Positives = 146/227 (63%), Gaps = 30/227 (13%)

```



```

Query: 24 LFNLDS-----VNGDDS-WLYEDIQLERGNGLGFSIAGGTDNPHIGTDTSIYITKLIS 76      (SEQ ID NO:283)
          L N DS      VNG D+ + YE+I LERGNGLGFSIAGGTDNPHIG D+SI+ITK+I+
Sbjct: 201 LVNTDSLETPTYVNGTDADYEYEEITLERGNGLGFSIAGGTDNPHIGDSSIFITKIIT 260      (SEQ ID NO:284)

Query: 77 GGAAAADGRLXXXXXXXXXXXXXXXXXXXXPHASAVDALKKAGNVVKLHVKRKXXXXXXXXXXXX 136
          GGAAA DGRL      H+ AV+ALK+AG++V+L+VKR+
Sbjct: 261 GGAAAQDGRRLRVNDCILQVNEVDVRDVTSHKAVEALKEAGSIVRLYVKKRKPVSE----- 315
Query: 137 XXXXXXXXXXXXXXXXVIEIDLKVGKGLGFSIAGGIGNQHIPGDNGIYVTKLTDGGRAQV 196

```

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Sbjct: 316 -----K++EI L+KG KGLGFSIAGG+GNQHIPGDN IYVTK+ +GG A
KIMEIKLIKPGKGLGFSIAGGVGNQHIPGDN SIYVTKIIEGGAHK 361

Query: 197 DGRLSIGDKLIAVRTNGSEKNLENTHELAVALTKSITDKVTLLIGK 243

DG+L IGDKL+AV + LE VTHE AV LK+ +D V L + K

Sbjct: 362 DGKLQIGDKLLAV---NNVCLEEVTHEEAVTALKNTSDFVYLKVAK 404

Score = 88.2 bits (217), Expect = 7e-16

Identities = 68/234 (29%), Positives = 95/234 (40%), Gaps = 43/234 (18%)

Query: 40 DIQLERGNISGLGFSIAGGTDNPHIGTDTSIYITKLISGGAAAADGRLXXXXXXXXXXXXX 99

+I+L +G GLGFSIAGG N HI D SIY+TK+I GGAA DG+L

(SEQ ID NO:285)

Sbjct: 319 EIKLIKPGKGLGFSIAGGVGNQHIPGDN SIYVTKIIEGGAHKDGKLQIGDKLLAVNNVC 378

(SEQ ID NO:286)

Query: 100 XXXXPHASAVDALKKAGNVVVKLVKRKXXXXXXXXXXXXXXXXXXXXXKVI----- 153

H AV ALK + V L V + V

Sbjct: 379 LEEVTHEEAVTALKNTSDFVYLKVAKPTSMYMNDGYAPPDITNSSSQPVDNHVSPSSFLG 438

Query: 154 -----EIDLKVGKGLGFSIAGGIGNQHIPGDN SIYVT 186

++ L +G GLGF+I GG + GI+++

Sbjct: 439 QTPASPARYSPVSKAVLGDEITREPRKVVLRGSTGLGFNIVGGEDGE-----GIFIS 492

Query: 187 KLTGGRAGQVDGRLSIGDKLIAVRTNGSEKNLENTHELAVALTKSITDKVTLLI 240

+ GG A + G L GD++I+V + +L +HE A A LK+ VT++

Sbjct: 493 FILAGGPADLSGELRKGDRIISV---NSVDLRAASHEQAAAALKNAGQAVTIV 542

Score = 70.1 bits (170), Expect = 2e-10

Identities = 47/141 (33%), Positives = 69/141 (48%), Gaps = 12/141 (8%)

Query: 432 MPALPVESNQTNRSQSPQRPQPSRYASTNVLAAPVPGTPRAVSTEDITREPTITIQK 491

+P LPV + T PQ P +T+ L TP V+ D E IT+++

(SEQ ID NO:287)

Sbjct: 176 IPVLPVPAENTVILPTIPQANPPPV-LVNTDSLE-----TPTYVNGTDADYEYEITLER 229

(SEQ ID NO:288)

Query: 492 GPQGLGFNIVGGEDG-----QGIYVSFILAGGPADLGSELKRGDQLLSVNNVNLTHATH 545

G GLGF+I GG D I+++ I+ GG A L+ D +L VN V++ TH

Sbjct: 230 GNSGLGFSIAGGTDNPHIGDDSSIFITKIITGGAAQDGRLRVNDICILQVNEVDVRDVTH 289

Query: 546 EEEAQALKTSGGVVTLAQYR 566

+A +ALK +G +V L + R

Sbjct: 290 SKAVEALKEAGSIVRLYVKRR 310

Score = 67.4 bits (163), Expect = 1e-09

Identities = 39/81 (48%), Positives = 49/81 (60%), Gaps = 6/81 (7%)

Query: 487 ITIQKGPQGLGFNIVGGEDGQ-----GIYVSFILAGGPADLGSELKRGDQLLSVNNVNL 540

I + KGP+GLGF+I GG Q IYV+ I+ GG A +L+ GD+LL+VNNV L

(SEQ ID NO:289)

Sbjct: 320 IKLIKPGKGLGFSIAGGVGNQHIPGDN SIYVTKIIEGGAHKDGKLQIGDKLLAVNNVCL 379

(SEQ ID NO:290)

Query: 541 THATHEEAQALKTSGGVVTL 561

THEEA ALK + V L

Sbjct: 380 EEVTHEEAVTALKNTSDFVYL 400

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CLUSTAL W (1.82) sequence alignment

[illegible]

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Drosophila WVPSKESL 960
Human WVPAKEKL 926
 ***:.**

REPLACEMENT SHEET

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FIGURE 6C

Sequence alignment of Dros Dlg1 and Hu Dlg homolog 2

BLASTP sequence alignment

Score = 621 bits (1601), Expect = e-176

Identities = 318/524 (60%), Positives = 390/524 (73%), Gaps = 43/524 (8%)



```

Query: 438 ESNQTNNRSQSPQRPQPGSRYASTNVLAAPPPTPRAVSTEDITREPRTITIQKGPQGLG 497      (SEQ ID NO:259)
      +S T++ S RQP RAVS E EPR + + KG GLG
Sbjct: 389 DSEMTSHSQHSTATRQPSMTLQ-----RAVSLEG---EPRKVVVLRHKGSTGLG 432      (SEQ ID NO:292)

Query: 498 FNIVGGEDGQGIYVSFILAGGPADLGSSELKRGDQLLSVNNVNLTHATHEEAAQALKTSGG 557
      FNIVGGEDG+GI+VSFILAGGPADL EL+RGDQ+LSVN ++L A+HE+AA ALK +G
Sbjct: 433 FNIVGGEDGEGIFVSFILAGGPADLSGELQRGDQILSVNGIDLRGASHEQAAAALKGAGQ 492

Query: 558 VVTLAQAQYRPEEYNRFEARIQELKQXXXXXXXXXXXXXXXXX-QKRSLYVRALFDYDPNRD 616
      VT++AQY+PE+Y RFEA+I +L++Q QKRSLYVRA+FDYD ++D
Sbjct: 493 TVTIIAQQPEDYARFEAKIHDLREQMMNHSMSGSGSLRTNQKRSLYVRAMFDYDKSKD 552

Query: 617 DGLPSRGLPFKHGDILHVTNASDDEWWQARRVLGDNEDEQIGIVPSKRRWERKMRARDS 676
      GLPS+GL FK+GDILHV NASDDEWWQARRV+ + + E++G++PSKRR ERK RAR ++
Sbjct: 553 SGLPSQGLSFYKGDILHVINASDDEWWQARRVMLEGDSEEMGVIPSKRRVERKERARLKT 612

Query: 677 VKFQGHAAANNLNDKQSTLDRKKKNFTFSRKFPFMKSRDEKNEDGSDQEPNGVVSSTSEI 736
      VKF ++ K S D++KK+F FSRKFPP K++++ ++ SD E +
Sbjct: 613 VKFNAKPGVIDS--KGSFNDKRKKSFIKSRKFPFYKNKEQSEQETSDPE-----RGQE 663


Query: 737 DIXXXXXXXXXXXXXXXXXXVLSYEAVQRLSINYTRPVIILGPLKDRINDDLISEYDPKFG 796
      D+ +LSYE V R INYTRPVIILGP+KDRINDDLISE+PKFG
Sbjct: 664 DL-----ILSYEPVTRQEINYTRPVIILGPMKDRINDDLISEFPDKFG 706

Query: 797 SCVPHTTRPKREYVDGRDYHFVSSREQMERDIQNHLEAGQYNDNLYGTSVASVREVA 856
      SCVPHTTRPKR+YEVVDGRDYHFV SREQME+DIQ H FIEAGQYNDNLYGTSV SVR VA
Sbjct: 707 SCVPHTTRPKRDYEVVDGRDYHFVISREQMEKDIQEHKFIAGQYNDNLYGTSVQSVRFVA 766

Query: 857 EKGKHCILDVSGNAIKRLQVAQLYPVAVFIKPKSVDSVMEMNRRMTEEQAQKTYERAIAKM 916
      E+GKHCILDVSGNAIKRLQVAQLYP+A+FIKP+S++S+MEMN+R+TEEQAQKTY+RAIK+
Sbjct: 767 ERGKHCILDVSGNAIKRLQVAQLYPIAIFIKPRSLESLEMEMNKRLEEQAKKTYDRAIKL 826

Query: 917 EQEFGEYFTGVVQGDTIEEIYSKVKSMIWSQSGPTIWVPSKESL 960
      EQEFGEYFT +VQGDT+E+IY++ K +I QSGP IW+PSKE L
Sbjct: 827 EQEFGEYFTAIVQGDTLEDIYNQCKLVIEEQSGPFIWIPSKEKL 870
Score = 197 bits (502), Expect = 7e-49
Identities = 111/221 (50%), Positives = 140/221 (63%), Gaps = 24/221 (10%)

```



```

Query: 23 SLFNLDSVNGDD-SWLYEDIQLERGNGLGFSIAGGTDNPHIGTDTSIYITKLISGGAAA 81      (SEQ ID NO:293)
      +L + VNG + + +E+I LERGNGLGFSIAGGTDNPHIG D I+ITK+I GGAAA
Sbjct: 80 TLDTPYVNGTEIYEFEEITLERGNGLGFSIAGGTDNPHIGDDPGIFITKIIPGGAAA 139      (SEQ ID NO:294)

Query: 82 ADGRLXXXXXXXXXXXXXXXXXPHASAVDALKKAGNVVVLHVKKXXXXXXXXXXXXXXXXX 141
      DGRL H+ AV+ALK+AG++ +L+V+R+
Sbjct: 140 EDGRLRVNDCILRVNEVDVSEVSHSKAVEALKEAGSIARLYVRRRRPILET----- 190

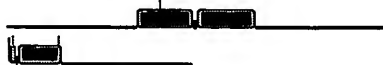
```

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Query: 142 XXXXXXXXXXXXVIEIDLKGGKGLGFSIAGGIGNQHIPGDNGIYVTKLTDGGRAQVDGRLS 201
V+EI L KG KGLGFSIAGG+GNQHIPGDN IYVTK+ DGG AQ DGRL
Sbjct: 191 -----VVEIKLFKGPGLGFSIAGGVGNQHIPGDNSIYVTKIIDGGAAQKDGRQLQ 240

Query: 202 IGDKLIAVRTNGSEKNLENVTHELAVATLKSITDKVTLIIG 242
+GD+L+ V + +LE VTHE AVA LK+ ++ V L +G
Sbjct: 241 VGDRLLMV---NNYSLEEVTHEEAVAILKNTSEVVYLKVG 277
Score = 66.2 bits (160), Expect = 3e-09
Identities = 40/125 (32%), Positives = 64/125 (51%), Gaps = 11/125 (8%)



Query: 448 SPQPRQPGSRYASTNVLAAPPGTPRAVSTEDITREPTITIQKGPQGLGFNIVGGEDGQ 507 (SEQ ID NO:295)
SP P +T+ L +P V+ +I E IT+++G GLGF+I GG D
Sbjct: 65 SPLKASPAPIIVNTDTLDTIP-----YVNGTEIEYEFEEITLERGNSGLGFSIAGGTDNP 119 (SEQ ID NO:296)

Query: 508 -----GIYVSFILAGGPADLGSELKRGDQLLSVNNVNLTHATHEEAAQALKTSGGVVTL 561
GI+++ I+ GG A L+ D +L VN V+++ +H +A +ALK +G + L
Sbjct: 120 HIGDDPGIFITKIIPGAAAEDGRLRVNDCILRVNEVDVSEVSHSKAVEALKEAGSIARL 179

Query: 562 LAQYR 566
+ R
Sbjct: 180 YVRRR 184
Score = 65.5 bits (158), Expect = 5e-09
Identities = 38/81 (46%), Positives = 47/81 (57%), Gaps = 6/81 (7%)



Query: 487 ITIQKGPQGLGFNIVGGEDGQ-----GIYVSFILAGGPADLGSELKRGDQLLSVNNVNL 540 (SEQ ID NO:297)
I + KGP+GLGF+I GG Q IYV+ I+ GG A L+ GD+LL VNN +L
Sbjct: 194 IKLFGKPGKGLGFSIAGGVGNQHIPGDNSIYVTKIIDGGAAQKDGRQLQVGDRLLMVNNYSL 253 (SEQ ID NO:298)

Query: 541 THATHEEAAQALKTSGGVVTL 561
THEEA LK + VV L
Sbjct: 254 EEVTHEEAVAILKNTSEVVYL 274
Score = 50.8 bits (120), Expect = 1e-04
Identities = 33/87 (37%), Positives = 48/87 (54%), Gaps = 10/87 (11%)



Query: 154 EIDLKGGKGLGFSIAGGIGNQHIPGDNGIYVTKLTDGGRAQVDGRLSIGDKLIAVRTNG 213 (SEQ ID NO:299)
++ L KG GLGF+I GG + GI+V+ + GG A + G L GD+++V NG
Sbjct: 421 KVV LHKGSTGLGFNIVGGEDGE-----GIFVFSFILAGGPADLSGELQRGDQILSV--NG 472 (SEQ ID NO:300)

Query: 214 SEKNLENVTHELAVATLKSITDKVTLI 240
+ L +HE A A LK VT+I
Sbjct: 473 ID--LRGASHEQAAAALKGAGQTVTII 497
Score = 41.2 bits (95), Expect = 0.10
Identities = 24/81 (29%), Positives = 36/81 (43%), Gaps = 6/81 (7%)



Query: 41 IQLERGNISGLGFSIAGGTDNPHIGTDTSIYITKLISGGAAAADGRLXXXXXXXXXXXXX 100 (SEQ ID NO:301)
+ L +G++GLGF+I GG D I+++ ++GG A G L
Sbjct: 422 VVLHKGSTGLGFNIVGGEDG-----EGIFVFSFILAGGPADLSGELQRGDQILSVNGIDL 475 (SEQ ID NO:302)

Query: 101 XXXPHASAVDALKKAGNVVKL 121
H A ALK AG V +
Sbjct: 476 RGASHEQAAAALKGAGQTVTI 496

REPLACEMENT SHEET

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FIGURE 6D

CLUSTAL W (1.82) sequence alignment

```

Drosophila  -----MTTRKKKRDGG----- 11      (SEQ ID NO:261)
Human       MFFACYCALRTNVKKYRQDEDAPHDHSLPRLTHEVRGPPELVHVSEKNLSQIENVHGYVL 60      (SEQ ID NO:303)
              * . * * *

Drosophila  -----GSGGGFIKKVSSLFNLDVNG-DDSWLYEDIQLERGNGLGFSIAGGTDNPH 62
Human       QSHISPLKASPAPIIVNTDTLDTIPYVNGTEIEYEFEEITLERGNGLGFSIAGGTDNPH 120
              * . : * : : * : : * * * : : : * * * * * * * * * * * * * * * *

Drosophila  IGTDTSIYITKLISGGAAAADGRLSINDIIVSVNDVSVVDVPHASAVDALKKAGNVVKLH 122
Human       IGDDPGIFITKII PGGAAEDGRLRVNDCILRVNEVDVSEVSHSKAVEALKEAGSIARLY 180
              ** * . : * * * * * * * * * * * * * * * * * * * * * * * * * * * *

Drosophila  VKRKRGTATTTPAGSAAGDARDSAASGPKVIEIDLKGGKGLGFSIAGGIGNQHIPGDNG 182
Human       VRRRRPILET-----VVEIKLFKGPGLGFSIAGGVGNQHIPGDNS 221
              * : * * * * * * * * * * * * * * * * * * * * * * * * * * *

Drosophila  IYVTKLTGGRAQVDGRLSIGDKLIAVRTNGSEKNLENVTHELAVATLKSITDKVTLIIG 242
Human       IYVTKIIDGGAAQKDGRQLVGDRLLMVNN---YSLEEVTHEEAVAILKNTSEVVYLKVG 277
              * * * * * * * * * * * * * * * * * * * * * * * * * * * *

Drosophila  KTQHLTTSASGGGGGGLSSGQQLSQSQSLATSQSQSVHQQQHATPMVNSQSTGALNSM 302
Human       NPPTIYMTDPYGP-----PDITHS-----YSPPMEN----- 303
              : . : : * : : : * : : * * *

Drosophila  GQTVVDSPSIPQAAA AVAAAANASASASVIASNTISNTT VTTVTATATASNDSSKLPPS 362
Human       -----HLLSGNN-----GTLEYKTSLPPIS 323
              : : : * * * . * . : * * *

Drosophila  LGANSSISISNSNSNSNNINNINSINNNSSSSSTTATVAATPTAASAAAAAASSPP 422
Human       PGRYSPIPKHMVLDDDYTRPPEPVYSTVNKLCDKP-----ASPRHYPVECDKSFL 375
              * * . * . : : : * * : . . . * * * * . *

Drosophila  ANSFYNNASMPALPVESNQTNNSRSQSPQPRQPGSRYASTNVLAAPPGTPRAVSTEDITR 482
Human       S-APYSHYHLGLLP-DSEMTSHSQHSTATRQP-----SMTLQRAVSLE---G 417
              : : * . : * * : * : : * . * * * * * * * * * *

Drosophila  EPRTITIKGPQGLGFNIVGGEDGQGIYVSFILAGGPADLGSELKRGDQLLSVNNVNLTH 542
Human       EPRKVVLHKGSTGLGFNIVGGEDGEGIFVSFILAGGPADLGSELQRGDQILSVNGIDL 477
              * * . : : * * * * * * * * * * * * * * * * * * * * * * * * *

Drosophila  ATHEEAAQALKTSGGVVTLQAQYRPEEYNRFEARIQELKQQAALGAGGSGT-LLRTTQKR 601
Human       ASHEQAAAALKGAGQTVTIIAQYQPEDYARFEAKIHDREQMMNHSMSGSLRTNQKR 537
              * : * * * * * * * * * * * * * * * * * * * * * * * * * * *

Drosophila  SLYVRALFDYDPNRDDGLPSRGLPFKHGDIHVTNASDDEWWQARRVLGDNEDEQIGIVP 661
Human       SLYVRAMFDYDKSKDGLPSQGLSFKYGDILHVINASDDEWWQARRVLEGDSEEMGVIP 597
              * * * * * * * * * * * * * * * * * * * * * * * * * * * *

Drosophila  SKRRWERKMRARDSVKFQGHAAANNLQKSTLDRKKKNFTFSRKFPFMKSRDEKNE 721
Human       SKRRVERKERARLKTVKFNAKPGVID--SKGSFNDKRKKSFIKSRKFPFYKNKEQSE 655
              * * * * * * * * * * * * * * * * * * * * * * * * * * *

Drosophila  SDQEPNGVVSSTSEIDINN VNNNQSNQSENVLSYEAQRLSINYTRPVIILGPLKD 781
Human       SDPE-----RGQEDLILSYEPVTRQEINYTRPVIILGPMKD 691
              * * * : * : * * * * * * * * * * * * * * * *

Drosophila  RINDDLISEYDPDKFGSCVPHTTRPKREYEV DGRDYHFVSSREQMERDIQNHLFIEAGQYN 841
Human       RINDDLISEYDPDKFGSCVPHTTRPKRDYEV DGRDYHFVISREQMEKDIQEHKFIEAGQYN 751
              * * * * * * * * * * * * * * * * * * * * * * * * * * *

Drosophila  DNLYGTSVASVREVAEKGKHCILDVSGNAIKRLQVAQLYPVAVFIKPKSVDSVMEMNRRM 901
Human       DNLYGTSVQSVRFVAERGKHCILDVSGNAIKRLQVAQLYPIAIFIKPRSLESLEMMNKRL 811
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Drosophila  TEEQAKKTYERAIKMEQEFGEYFTGVVQGD TIEEISYKVKSMIWSQSGPTIWPVSKESL 960
Human       TEEQAKKTYDRAIKLEQEFGEYFTAIVQGD TLEDIYNQCKLVIEEQSGPFIWIPSKEKL 870
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Hu-Dlg1	---MPVRKQDTQRALHLLLEEYRSKLSQTEDRQLRSSIERVINIFQSNLFQ-ALIDIQEFY	56	(SEQ ID NO:267)
Hu-Dlg4	---MSQRPRAPRSALWLLAPPLLRWAPP-----LLTVLHSDLFQ-ALLDILDY	45	(SEQ ID NO:304)
Hu-Dlg2	---MFFACYCALRTNVKKYRQDEAPHDHS-----LPRLLTVHVRGP-ELVHVSEK-	47	(SEQ ID NO:303)
Hu-Dlg3	MHKHQHCCKCPECYEVTRLAALRRLEPPGYG-----DWQVPDPYGPGGGNGASAGYGGYS	55	(SEQ ID NO:305)
Dm-Dlg1	---MTTRKK-----KRDGG-----	11	(SEQ ID NO:259)
Hu-Dlg5	-----		(SEQ ID NO:306)

Hu-Dlg1	EVTLILDNPKCIDRSKPSSEPIQPVNTWEISSLPSSVTVTSETLPSSLSPSVEKYRYQDEDT	116
Hu-Dlg4	EASLSES-----KQYRYQDEDT	63
Hu-Dlg2	NLSQIEN-----VHGYVLSHIS	66
Hu-Dlg3	SQTLPSQAG-----ATPTPRTKAKLIP	77
Dm-Dlg1	-----	
Hu-Dlg5	-----	

Hu-Dlg1	PQEHI SP QITNEVIGPELVHVSEKNLSEIENVHGFVSHSHISPIKPT E AVLPSPTVPVI	176
Hu-Dlg4	PLEHSP-----AHLPN-----	74
Hu-Dlg2	LK-----	68
Hu-Dlg3	TGRDVG-----PVPLKPVP G K-----	93
Dm-Dlg1	-----	
Hu-Dlg5	-----	

Hu-Dlg1	PVLVPVAENTVILPTIPQANPPPLVNTDSLETP---TYVNGTDADYEYEEITLERGNSG	233
Hu-Dlg4	-----QANSPPIVNTDTLEAPGYELQVNGTEGEMEYEEITLERGNSG	117
Hu-Dlg2	-----ASPAPIVNTDTLDTIP---YVNGTEIEYEFEEITLERGNSG	107
Hu-Dlg3	-----STPKLNGSGPSWPECTCTNRDWYEQVNGSDGMFKYEEIVLGRNSG	140
Dm-Dlg1	-----GSGGGFIKKVSSLFNLD---SVNGDD-SWLYEDIQLERGNSG	49
Hu-Dlg5	-----MRATHGSNSLPSSARLGSSSN	21

Hu-Dlg1	LGFSIAGGTDNPHIGDDSSIFITKIIITGGAAQDGLRLVNDCILQVNEVDVRDVTTHSKAV	293
Hu-Dlg4	LGFSIAGGTDNPHIGDDPSIFITKIIIPGGAAQDGLRLVNDISILFVNEVDVREVTHSAAV	177
Hu-Dlg2	LGFSIAGGTDNPHIGDDPGIFITKIIIPGAAEDGRLRVNDICILRVNEVDVSEVSHSKAV	167
Hu-Dlg3	LGFSIAGGTDNPHVDDPGIFITKIIIPGAAAMDGRGLGVNDICVLRVNEVEVSEVSHSRV	200
Dm-Dlg1	LGFSIAGGTDNPHITGTDTSIYITKLSGGAAADGRLSINDIIVSVNDVSVVDVPHASAV	109
Hu-Dlg5	LQFKAER-IKIPSTPRYPRSVVGSR--GSVSHSECSTPPQSPNLIDTLLSSCSQSQTSSA	78
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Hu-D1g1      EALKEAGSIVRLYVKRRK-----PVS-----EKIMEIKLIKGPKGLGFSI 333
Hu-D1g4      EALKEAGSIVRLYVMRRK-----PPA-----EKVMEIKLIKGPKGLGFSI 217
Hu-D1g2      EALKEAGSIARLYVRRR-----PIL-----ETVVEIKLFKGPKGLGFSI 207
Hu-D1g3      EALKEAGPVVRLVVRRRQ-----PPP-----ETIMEVNLKFGPKGLGFSI 240
Dm-D1g1      DALKKAGNVVKLHVKKRK-GTATTPAAGSAAGDARDSAASGPKVIEIDLVGKGGKGLGFSI 168
Hu-D1g5      TLPRIAVNPASLGGERRKDR---PYV-----EEPRHVKVQKGSSEPLGISI 119

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Hu-Dlg1      AGGVGNQHIPGDN SIYVTK IIEGGA AHKDGK LQIGDK LLAVNN ---- VCLEEV THEEAVT 389
Hu-Dlg4      AGGVGNQHIPGDN SIYVTK IIEGGA AHKDGRL QIGDK ILAVNS ---- VGLEED VMHEDAVA 273
Hu-Dlg2      AGGVGNQHIPGDN SIYVTK IDGGA AQKDR LQVGD RLLMVNN ---- YSLEEV THEEAVA 263
Hu-Dlg3      AGGIGNQHIPGDN SIYTKI IIEGGA AQKDGRL QIGDR LLAVNN ---- TNLQDV RHEEAVA 296
Dm-Dlg1      AGGIGNQHIPGDN GIYVTK LT DGGRA QVDGR L SIGDK LIAVRT NGSEKN LENV THELAVA 228
Hu-Dlg5      VSGE----- KGGIY SVSKVT VSGIA HQAG -LEYGD QLLEFNG ---- INLRSATE QQARL 167

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Hu-D1g1	ALKNTSDFVYLKVAKPTSMYMNDGYA-----	415
Hu-D1g4	ALKNTYDVVYLKVAKPSNAYLSDSYA-----	299
Hu-D1g2	ILKNTSEVVYLKVGNPPTTIYMTDPYG-----	289
Hu-D1g3	SLKNTSDMVYLKVAKPGSLHLNDMYA-----	322
Dm-D1g1	TLKSIITDKVTLIIGKTKQLHTTSASGGGGGGLSSGQQLSQSQSQLATSQSQSQVHQQQHAT	288
Hu-D1g5	IIGQQCDTITILAQYNPHVHQLSSHS-----	193

Hu-Dlg1 -----
 Hu-Dlg4 -----
 Hu-Dlg2 -----
 Hu-Dlg3 -----
 Dm-Dlg1 PMVNSOSTGALNSMGOTVVDSPSIPQAAAAVAAAAANASASASVIASNNTISNTTIVTTVTA 348

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[illegible]

REPLACEMENT SHEET

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Hu-Dlg1 KGKHCILDVSGNAIKRLQIAQLYPISIFIKPKSMENIMEMNK-----RLTEEQARKTFE 877
 Hu-Dlg4 QGKHCILDVGSANAVRRLQAHLHPIAIFIRPRSLENVLEINK-----RITEEQARKAFD 718
 Hu-Dlg2 RGKHCILDVSGNAIKRLQVAQLYPIAIFIKPRSLESLEMEMNK-----RLTEEQAKKTYD 821
 Hu-Dlg3 RGKHCILDVSGNAIKRLQQAQLYPIAIFIKPKSIEALMEMNR-----RQTYEQANKIYD 768
 Dm-Dlg1 KGKHCILDVSGNAIKRLQVAQLYPVAVFIKPKSVDSVMEMNR-----RMTEEQAKKTYE 911
 Hu-Dlg5 KNRHCLLDIAPHAIERLHHMHYPIVIFIFIHYKSAKHIKEQRDPYLRDKVTQRHSKEQFE 626
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Hu-Dlg1 RAMKLEQEFTEHFTAIVQGDITLEDIYNQVKQIIEEQSGSYIWVPAKEKL 926
 Hu-Dlg4 RATKLEQEFTECFSAIVEGDSFEEIYHKVVRVIEDLSGPYIWVPARERL 767
 Hu-Dlg2 RAIKLEQEFGEYFTAIVQGDITLEDIYNQCKLVIEEQSGPFIWIPSEKL 870
 Hu-Dlg3 KAMKLEQEFGEYFTAIVQGDSLEEIYNKIKQIIEEQSGHYIWVPSPEKL 817
 Dm-Dlg1 RAIKMEQEFGEYFTGVVQGDITIEEIYSKVKSMIWSQSGPTIWVPSKESL 960
 Hu-Dlg5 AAQKLEQEYSRYFTGVIQGGALSSICTQILAMVNQEONKVLWIPACPL- 674
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